

[illegible]

2450	2460	2470	2480	2490	2500	2510	2520
AAGGGAAGAAACCCAGATTGGTGAAGCTGTGACAGCTTCTTGACAAAGGATGACAGAGAGGACC							
AAGGGAAGAAACCCAGATTGGTGAAGCTGTGACAGCTTCTTGACAAAGGATGACAGAGAGGACC	2460	2470	2480	2490	2500	2510	2520

CTCTACCTGGG
 |||||
 CTCTACCTGGG
 2530

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2. US-09-579-543-13 (1-2531)
   US-09-579-543-14 Sequence 14, Application US/09579543
       -al Score      =    2536 Optimized score =    2526 Significance = -0.57
Residue Identity =    99% Matches           =    2526 Mismatches =     .5
Gaps              =     0 Conservative Substitutions =     0

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[illegible]

GCCACGCTTTGGCTGACACTCTGGCTCTCTGCCCTGAGAGAGTCATCAGTCACTGTCAGTCTTCTGTGACGAGAGACTGAG
 580 590 600 610 620 630 640
 650 660 670 680 690 700 710 720
 CACTGCAGCGCTGTAGAGAGCGCTTGAGGCCCAAGAGAGGCCCTTGCGCTGTGGTCTCAACGCGCTCTACT
 CACTGCAGCGCTGTAGAGAGCGCTTGAGGCCCAAGAGAGGCCCTTGCGCTGTGGTCTCAACGCGCTCTACT
 650 660 670 680 690 700 710 720

ACTGAGGACGAGGAGGCTCTCCTCCCTCCTCCTCCTCGCCGTGGCACCCGCGAAGAATGTCCTGT
730 740 750 760 770 780 790

ATTGAGGACGAGGAGGCTCTCCTCCCTCCTCCTCCTCGCCGTGGCACCCGCGAAGAATGTCCTGT
730 740 750 760 770 780 790

ACTGAGGACGAGGAGGCTCTCCTCCCTCCTCCTCCTCGCCGTGGCACCCGCGAAGAATGTCCTGT
730 740 750 760 770 780 790

800 810 820 830 840 850 860
GCTGATGACACAGGTTCTTCCCGAGATGCTCTAGGAGAGCTCTGTGCTTACCCACTACCAATCACCTTCACTTGC
GCTGATGACACAGGTTCTTCCCGAGATGCTCTAGGAGAGCTCTGTGCTTACCCACTACCAATCACCTTCACTTGC
GCTGATGACACAGGTTCTTCCCGAGATGCTCTAGGAGAGCTCTGTGCTTACCCACTACCAATCACCTTCACTTGC
GCTGATGACACAGGTTCTTCCCGAGATGCTCTAGGAGAGCTCTGTGCTTACCCACTACCAATCACCTTCACTTGC

870 880 890 900 910 920 930
TGGGGCCACCCATATAGGGTTCACGACCCAGAGAGGAGGGGCCCAACACCTCGCTGACGGAGAGTCC
TGGGGCCACCCATATAGGGTTCACGACCCAGAGAGGAGGGGCCCAACACCTCGCTGACGGAGAGTCC
870 880 890 900 910 920 930

940 950 960 970 980 990 1000
TTGTTCGAGAACACTCAGTATACAAGTGGATGTGATTCCTCTTTTCGTCCCGCAAGTATCAGGCCAAG
TTGTTCGAGAACACTCAGTATACAAGTGGATGTGATTCCTCTTTTCGTCCCGCAAGTATCAGGCCAAG
TTGTTCGAGAACACTCAGTATACAAGTGGATGTGATTCCTCTTTTCGTCCCGCAAGTATCAGGCCAAG
940 950 960 970 980 990 1000

1010	1020	1030	1040	1050	1060	1070	1080
GAGCTGCTCACC	AAAGCAGAAATG	CTGGAGAGAGT	CATCAAAATTT	ACAAGCGCTG	TTTCCGTGAT	CTTTT	
1010	1020	1030	1040	1050	1060	1070	1080
GAGCTGCTCACA	AAAGCAGAAATG	CTGGAGAGAGT	CATCAAAATTT	ACAAGCGCTG	TTTCCGTGAT	CTTTT	
1010	1020	1030	1040	1050	1060	1070	1080
GAGCTGCTCACA	AAAGCAGAAATG	CTGGAGAGAGT	CATCAAAATTT	ACAAGCGCTG	TTTCCGTGAT	CTTTT	

GGCAAAGCCTCCGAGTCCCTCGAAGATGATCTTTGGCATTTGAACGTGAAGAAATGGAACCGCCGCGCATGACATACC	1090	1100	1110	1120	1130	1140	1150
GGCAAAGCCTCCGAGTCCCTCGAAGATGATCTTTGGCATTTGAACGTGAAGAAATGGAACCGCCGCGCATGACATACC	1090	1100	1110	1120	1130	1140	1150

TACACCTTGTACACTCCCGGGCTTTCCATGATGGCTGCTGGGTAAATATCAGATCTTCCCAAGAC	1160	1170	1180	1190	1200	1210	1220
TACACCTTGTACACTCCCGGGCTTTCCATGATGGCTGCTGGGTAAATATCAGATCTTCCCAAGAC	1160	1170	1180	1190	1200	1210	1220
TACACCTTGTACACTCCCGGGCTTTCCATGATGGCTGCTGGGTAAATATCAGATCTTCCCAAGAC	1160	1170	1180	1190	1200	1210	1220

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1300	1310	1320	1330	1340	1350	1360
GAGCTGGGTGTGATGGGGGGGTATGATGGAGGGAGCACTGTCTATGGGGAGCCAGGAAACTGCTACAC						
1300	1310	1320	1330	1340	1350	1360
GAGCTGGGTGTGATGGGGGGGTATGATGGAGGGAGCACTGTCTATGGGGAGCCAGGAAACTGCTACAC						

1370	1380	1390	1400	1410	1420	1430	144
CAAGATTGGGTCGAGAAACTACTCTGATACCGGACAGTACCCGGATACGCGGTATGAGATT							
CAAGATTGGGTCGAGAAACTACTCTGATACCGGACAGTACCCGGATACGCGGTATGAGATT							
1370	1380	1390	1400	1410	1420	1430	144

	1450	1460	1470	1480	1490	1500	1510
CCTGTTGGGTCCAAAGGCCTTGTGCTGAACCAAGTCATGTAACAAGTCTTGAGCAGCATGTGGTCAAGGCTCAATTGCC							
CGTGTGGGTGCCAAGGGCTCTGCTGGAACACAGTCATGTGAAGAATCCTGTAGACCATGTGGTCAAGGGTCAAATCC							

